

Sphingononas ORF1

ATG	ACC	GAT	CCA	CGT	CAG	CTG	CAC	CTG	GCC	GGC	TTC	TTC	TGT	GCC	GGC	AAC	GTC	ACG	CAC	
M	T	D	P	R	Q	L	H	L	A	G	F	F	C	A	G	N	V	T	H>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
90																				
GCC	CAC	GGG	GGG	TGG	CGC	CAC	GGG	GAC	TCC	AAC	GGG	TTC	TTC	CTC	ACC	AAG	GAG	TAC	TAC	
A	H	G	A	W	R	H	A	D	S	N	G	F	L	T	R	E	Y	Y>		
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
150																				
CAG	CAG	ATT	GCC	CGC	ACG	CTC	GAG	CCC	GGC	AAG	TTC	GAC	CTG	CTG	TTC	CTT	CCC	GAC	GCG	
Q	Q	I	A	R	T	L	E	R	G	K	F	D	L	L	F	L	P	D	A>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
210																				
CTC	GCC	GTG	TGG	GAC	AGC	TAC	GGC	GAC	AAT	CTG	GAG	ACC	GTC	CTG	TAT	GCG	GCG	CAA		
L	A	V	W	D	S	Y	G	D	N	L	E	T	G	L	R	Y	G	G	Q>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
270																				
GGC	GGG	GTG	ATG	CTG	GAG	CCC	GGC	GTC	GTA	GTT	ATC	GCC	GCG	ATG	GCC	TCG	GTC	ACC	GAA	CAT
G	A	V	M	L	E	P	G	V	V	I	A	A	M	A	S	V	T	E	H>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
330																				
CTG	GGG	CTG	GGC	GCC	ACC	ATT	TCC	ACC	TAC	TAC	CCG	CCC	TAC	CAT	GTA	GCC	CGG	GTC		
L	G	L	G	A	T	I	S	T	T	Y	Y	P	P	Y	H	V	A	R	V>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
390																				
GTC	GCT	TCG	CTG	GAC	CAG	CTG	TCC	TCC	GGG	CGA	GTG	GTG	TGG	AAC	GTC	ACC	TCG	CTC		
V	A	S	L	D	Q	L	S	S	G	R	V	S	W	N	V	V	T	S	L>	
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*		

FIGURE 1A

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Sphingomonas ORF1 (cont)

AGC AAT GCA GAG GCG CGC AAC TTC GGC TTC GAT GAA CAT CTC GAC CAC GAT GCC CGC CGC TAC	450
S N A E A R N F G D E H L D K D A R Y>	
GAT CGC CCC GAT GAA TTC CTC GAG GTC GTG CGC AAG CTC TGG AAC AGC TGG GAT CGC GAT	540
D R A D B F L E V V R K L W N S W D R D>	
GCG CTG ACA CTC GAC AAG GCA ACC ACC CAG TTC GGC GAT CGC GCT AAG GAG GTG CGC TAC ATC	600
A L T L D K A T G Q F A D P A K V R Y I>	
GAC CAC CGC GGC GAA TGG CTC AAC GTA CGC GGG CCG CTT CAG GTG CGC TCC CGC CCC CGC	630
D H R G E W L N V R G P L Q V P R S P Q>	
GCG GAG CCT GTC ATT CTG CAG GCC GGG CTT TCG GCG CGG CGC AAG CGC TTC GCC GGG CGC	660
G E P V I L Q A G L S A R G K R F A G R>	
TGG GCG GAC GCG GTG TTC ACG ATT TCG CGC AAT CTG GAC ATC ATG CAG GCC ACC TAC CGC	720
W A D A V F T I S P N L D I M Q A T Y R>	
GAC ATA AAG GCG CAG GTC GAG GCC GGC GGA CGC GAT CCC GAG CAG GTC AAG GTG TTT GCC	780
D I K A Q V E A A G R D P E Q V K V F A>	
	840

FIGURE 1B

Sphingomonas ORF1 (cont)

970	GGC GTG ATG CCG ATC CTC GGC GAG ACC GAG GCG ATC GCC AGG CAG CGT CTC GAA TAC ATA A V M P I L G E T A R Q R L E Y I>	*	*	*	*	*	*	200
970	AAT TCG CTG GTC CAT CCC GAA GTC GGG CTT TCT ACG TTG TCC AGC CAT GTC GGG GTC AAC N S L V H P E V G L S T L S S H V G V N>	*	*	*	*	*	*	960
990	CTT GCC GAC TAT TCG CTC GAT ACC CCC CTG ACC GAG GTC CTC GGC GAT CTC GCC CAG CGC L A D Y S L D T P L T E V L G D L A Q R>	*	*	*	*	*	*	1020
1050	AAC GTG CCC ACC CAA CTG GCC ATG TTC GCC AGG ATG TTG CAG GCC GAG ACG CTG ACC GTG N V P T Q L G M F A R M L Q A E T L T V>	*	*	*	*	*	*	1080
1110	GGA GAA ATG GGC CGG CGT TAT GGC GCC AAC GTG GGC TTC GTC CCG CAG TGG GCA ACC G E W G R R Y G A N V G F V P Q W A G T>	*	*	*	*	*	*	1140
1170	CGC GAG CAG ATC GCG GAC CTG ATC GAG ATC CAT TTC AAG GCC GGC GGC GAT GGC TTC R E Q I A D L I E T H P K A G G A D G F>	*	*	*	*	*	*	1200
1230	ATC ATC TCG CCG GCG TTC CTG CCC GGA TCT TAC GAG GAA TTC GTC GAT CAG GTG GTG CCC I I S P A F L P G S Y E E F V D Q V V V P>	*	*	*	*	*	*	1260

FIGURE 1C

### Sphingomonas ORF1 (cont)

ATC CTG CAG CAC CGC GGA CTG TTC CGC ACT GAT TAC GAA GGC CGC ACC CTG CGC AGC CAT	1220
I L Q H R G L F R T D Y E G R T L R S H >	
ATC CTG CGA CTG CGT GAA CCC GCA TAC CTG GGA GAG TAC GCA TGA	1290
L G L R E P A Y L G E Y A * >	
CTG CGA CTG CGT GAA CCC GCA TAC CTG GGA GAG TAC GCA TGA	1350
L G L R E P A Y L G E Y A * >	

FIGURE 1D

Sphingomonas ORF2

ATG	ACG	ACA	GAC	ATC	CAC	CCG	GGC	GCC	GGG	TCG	TCG	CCG	GGG	CGC	GGG	ACG	ATC	*	
M	T	T	D	I	H	P	A	S	A	S	P	A	A	R	A	T	I>	*	
ACC	TAC	AGC	AAC	TGC	CCC	GTG	CCT	AAT	GCC	CTG	CTG	CCC	GGC	CTG	GGC	TCA	GGT	ATT	CTG
T	Y	S	N	C	P	V	P	N	A	L	A	A	L	G	S	G	I	L>	
GAC	AGT	GCC	GGG	ATC	ACA	CTT	GCC	CTG	CTG	ACC	GGA	AAG	CAG	GGC	GAG	GTG	CAC	TTC	ACC
D	S	A	G	I	T	L	A	L	L	T	G	K	Q	G	E	V	H	F	T>
TAC	GAC	CGA	GAT	GAC	TAC	ACC	CGC	TTC	GGC	GGC	GAG	ATT	CCG	CCG	CTG	GTG	AGC	GAG	GGG
Y	D	R	D	Y	T	R	F	G	G	E	I	P	P	L	V	S	E	G>	
CTG	CGT	GCG	CGG	CGG	ACC	CGG	CTG	CTG	CGA	CTG	ACG	CCG	GTG	CTG	GGC	GGC	TGG	GGC	
L	R	A	P	G	R	T	R	I	L	G	L	T	P	V	L	G	R	W	
TAC	TTC	GTC	CGG	GGC	GAC	AGC	GGC	ATC	CGC	ACC	CCG	GAT	CTT	GCC	GGC	GGC	CCG	GTC	
Y	F	V	R	G	D	S	A	I	R	T	P	A	D	L	A	G	R	R	V>
GGA	GTA	TCC	GAT	TCG	GGC	AGG	AGG	ATA	TTG	ACC	GGG	AGG	CTG	GGC	GAC	TAC	GGC	GAA	CTT
G	V	S	D	S	A	R	R	I	L	T	G	R	L	G	D	Y	R	E	L>

FIGURE 2A

Sphingomonas ORF2 (cont)

GAT CCC TGG CCG CAG ACC CTC GCG CTC GCG CTC GCG ACA TGG GAG CGT GCC TTG CTG AGC	450	*	*	*	*	*	*	*	*
D P W R Q T L V A L G T W E A R A L L S>									
ACG CTC GAG ACG GCG GGG CTT GGC GTC GGC GAC GTC GAG CTG ACG CGC ATC GAG AAC CCG	510	*	*	*	*	*	*	*	*
T L E T A G L G V D V E L T R I E N P>									
TTC GTC GAC GTG CCG ACC GAA CGA CTG CAT GCC GCC CGC TGC CTC AAA GGA ACC GAC CTG	570	*	*	*	*	*	*	*	*
F V D V P T E R L H A A G S L K G T D L>									
TTC CCC GAC GTC ACC AGC CAG CAG GCC GCA GTC CTT GAG GAT GAG CGC GCC GAC GCC CTG	630	*	*	*	*	*	*	*	*
F P D V T S Q A A V L E D R A D A L>									
TTC GCG TGG CTT CCC TGG GCG GCC GAG CTC GAG ACC CGC ATC CGT GCA CGG CCG GTC CTA	690	*	*	*	*	*	*	*	*
F A W L P W A A E L E T R I G A R P V L>									
GAC CTC AGC GCA GAC GAC CGC AAT GCC TAT GCG AGC ACC TGG ACG CGT AGC GCC GAG CTG	750	*	*	*	*	*	*	*	*
D L S A D D R N A Y A S T W T V S A E L>									
CTG GAC CGG CAG CCC GAA CTG GTG CAG CGG CTC GTC GAT GCC GTG AGC GCC GAG CTG	810	*	*	*	*	*	*	*	*
V D R Q P E L V Q R L V D A V V D A G R>									

FIGURE 2B

### Sphingomonas ORF2 (cont)

FIGURE 2C

Sphingomonas ORF3

	10	*	20	*	30	*	40	*	50	*	60	*
M	N	E	L	V	K	D	L	G	L	N	R	S
ATG	AAC	GAA	CTC	GTC	AAA	GAT	CTC	GGC	CTC	AAT	CGA	TCC
R	L	A	A	Q	W	G	A	T	A	V	D	R
70	*	80	*	90	*	100	*	110	*	120	*	
CGA	CTG	GCC	GCG	CAG	TGG	GGG	GCC	ACC	GCT	GTT	GAT	CGG
T	A	E	L	D	Q	L	R	G	S	G	L	L
130	*	140	*	150	*	160	*	170	*	180	*	
ACC	GCC	GAA	CTC	GAT	CAA	CTG	CGC	GGC	AGC	GGC	CTG	CTG
T	A	E	L	D	Q	L	R	G	S	G	L	L
190	*	200	*	210	*	220	*	230	*	240	*	
TAT	GGC	GGC	TGG	GGC	GCC	GAC	TGG	CCA	ACG	ACT	CTG	GAA
Y	G	G	W	G	A	D	W	P	T	T	L	E
250	*	260	*	270	*	280	*	290	*	300	*	
GTG	GAC	GGA	TCG	CTG	GCG	CAT	CTA	TTC	GGC	TAC	CAC	CTC
V	D	G	S	L	A	H	L	F	G	Y	H	L
310	*	320	*	330	*	340	*	350	*	360	*	
CTG	TTC	GGC	TCG	GGC	CCA	AAG	GAA	CGG	CTG	TAC	CGC	CAG
L	F	G	S	A	P	Q	K	E	R	L	Y	R
370	*	380	*	390	*	400	*	410	*	420	*	
CGG	GTC	GGG	AAT	GCG	TCG	AGC	GAA	AAC	AGC	CAC	GTG	CTC
R	V	G	N	A	S	S	E	N	N	S	H	V

FIGURE 3A

Sphingomonas ORF3 (cont)						
430	440	450	460	470	480	*
*	*	*	*	*	*	*
ACC	GCC	GTC	GAT	GCC	GGG	TTC
T	A	V	D	G	G	GTC
K	S	S	D	L	I	CTC
490	*	*	*	*	*	*
AAA	AGC	TCC	GAC	CTG	CTC	ATC
A	I	T	A	V	I	GTG
550	*	*	*	*	*	*
GGG	ATC	ATC	ACC	GGC	GTC	ATT
R	A	I	T	A	V	CCC
610	*	*	*	*	*	*
CGC	GCA	ATC	GGG	ATG	CGC	CAG
R	A	I	G	M	R	ACC
670	*	*	*	*	*	*
TAC	CCA	GAC	GAG	ATC	TTC	GGG
Y	P	D	E	I	L	G
730	*	*	*	*	*	*
CGC	GGC	AGC	TGG	ACG	CCG	GCG
R	G	S	L	W	T	ATT
790	*	*	*	*	*	*
CGC	CGT	GGC	GGC	CTC	GAG	GGC
A	R	G	A	A	A	GAT

FIGURE 3B

## Sphingomonas ORF3 (cont)

	850	860	870	*	880	*	890	*	900	*
CCC	GCC	GGC	GTC	GCG	AAG	GCG	ACA	GAG	GAT	CCC
P	A	G	V	A	K	A	T	E	D	CAC
										ATC
										GCC
										ACC
										GGT
										GAA
										CTG
910	*	*	*	*	*	*	*	*	*	*
GCG	ATC	GCG	CTC	CAG	GGC	GGC	GCG	GCG	GTC	GCG
A	I	A	L	Q	G	A	E	A	A	GCC
										CAG
										CTG
										TTG
										CAA
										CAG
970	*	*	*	*	*	*	*	*	*	*
GCG	TGG	GAC	AAG	GGC	GAT	GCG	GTC	GCG	CAG	CTG
A	W	D	K	G	D	A	V	T	P	ATG
										GAA
										GAG
										GGC
										CAG
1030	*	*	*	*	*	*	*	*	*	*
TCG	GGT	GTC	GCC	CTC	TCG	ACG	AAG	GCC	GCC	CTC
S	G	V	K	A	L	S	T	K	A	GAC
										ATC
										ACC
										CGT
										ATT
										TTC
										GAG
1090	*	*	*	*	*	*	*	*	*	*
ACA	ACG	GGC	TCG	CGA	TCG	ACG	CAT	CCC	AGA	TAC
T	T	G	S	R	S	T	H	P	R	GGA
										TTC
										GAT
										CGG
										TGG
										CGT
1150	*	*	*	*	*	*	*	*	*	*
CGG	ACT	CAT	ACG	CTG	CAC	GAT	CCG	GTA	TCG	TAT
R	T	H	T	L	H	D	P	V	S	AAA
										ATC
										GTC
										GAT
										GTG
1210	*	*	*	*	*	*	*	*	*	*
CTC	AAC	GGG	ACA	TTC	CCG	GTT	CCC	GGA	TTT	ACG
L	N	G	T	F	P	V	P	G	F	T
										S>

FIGURE 3C

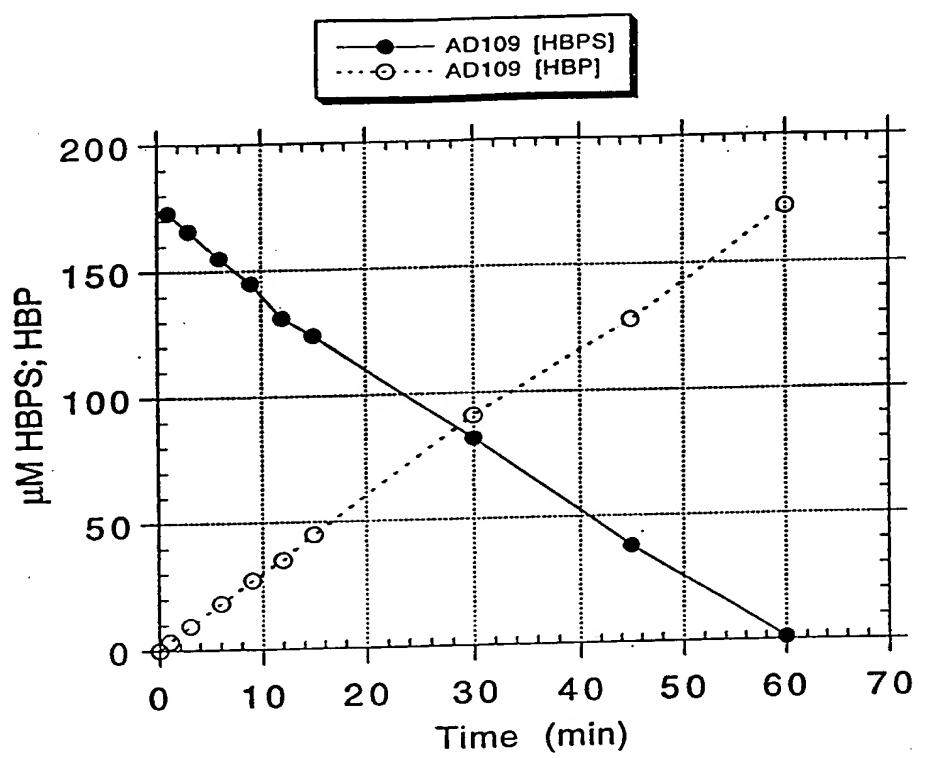


FIGURE 4

200 bp

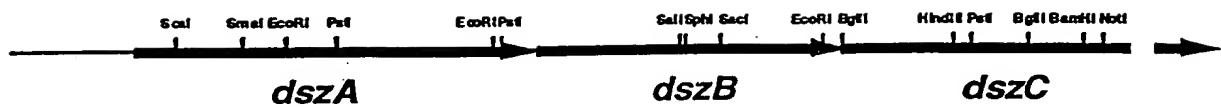


FIGURE 5

*Sphingomonas dsz* sequence

10	20	30	40	50	60
*	*	*	*	*	*
GGTTCGAGAT CGATCTGACC GTCGAACCCG GCGCGGTTCA AACCATCCTC TGGGGCCTCT					
CCAAGCTCTA GCTAGACTGG CAGCTTGGGC CGCGCCAAGT TTGGTAGGAG ACCCCGGAGA					
70	80	90	100	110	120
*	*	*	*	*	*
TCTTGCACCT GACATAGGAA TCTCTACTAA ATAAATAGAT ATTTATTGCA CACTAAGTTC					
AGAACGTGAA CTGTATCCTT AGAGATGATT TATTATCTA TAAATAAGCT GTGATTCAAG					
130	140	150	160	170	180
*	*	*	*	*	*
GGTGATCAGG CCGACCGTGT GTCTCAAGTG CTCGCTCCGG GTTGCCACGA GCTAAAGCGC					
CCACTAGTCC GGCTGGCAC AAGAGTTCAC GAGCGAGGCC CAACGGTGCT CGATTCGCG					
190	200	210	220	230	240
*	*	*	*	*	*
GCGATGCTGG GGCGACAGCG CTAGGCATTG CGTTCCCTCA CACCAATGAT GAGATGATAC					
CGCTACGACC CCGCTGTCGC GATCCGTAAC GCAAGGGAGT GTGGTTACTA CTCTACTATG					
250	260	270	280	290	300
*	*	*	*	*	*
GATGCGCATG ACCACTATCC GCACCTAGCA CGAAAGATCC GTGCATTTCG CGAATGCCAA					
CTACCGTAC TGGTGATAGG CGTGGATCGT GCTTTCTAGG CACGTAAAGC GCTTACGGTT					
310	320	330	340	350	360
*	*	*	*	*	*
TGAAGAGGAC CGACGTACGG CAGCTTCCTA CGCTTTCGCG CCATCGTTCA TAGCCAAGGT					
ACTTCTCCTG GCTGCATGCC GTCGAAGGAT GCGAAAGCGC GGTAGCAAGT ATCGGTTCCA					
370	380	390	400	410	420
*	*	*	*	*	*
CTTTTCGACG CCGGTTCGCG TGGGCGACTG ACGGGCGTAG CGCCGCGACT ATTGTTTCA					
GAAAAGCTGC GGCCAAGCGC ACCCGCTGAC TGCCGCCATC GCGGCGCTGA TAAGCAAAGT					
430	440	450	460	470	480
*	*	*	*	*	*
AACTCACGAG GATAAGAGCC TATGACCGAT CCACGTCAGC TGCACCTGGC CGGATTCTTC					
TTGAGTGCTC CTATTCTCGG ATACTGGCTA GGTGCAGTCG ACGTGGACCG GCCTAACAGAG					
490	500	510	520	530	540
*	*	*	*	*	*
TGTGCCGGCA ACGTCACCGCA CGCCCACGGG GCGTGGCGCC ACGCCGACGA CTCCAACGGC					
ACACGGCCGT TGCAGTGGCGT GCGGGTGCCT CGCACCGCGG TGCGGCTGCT GAGGTTGCCG					
550	560	570	580	590	600
*	*	*	*	*	*
TTCCTCACCA AGGAGTACTA CCAGCAGATT GCCCGCACGC TCGAGCGCGG CAAGTTCGAC					
AAGGAGTGGT TCCTCATGAT GGTGCTCAA CGGGCGTGCAG AGCTCGCGCC GTTCAAGCTG					

FIGURE 6A

*Sphingomonas dsz* sequence (page 2)

610	620	630	640	650	660
*	*	*	*	*	*
CTGCTGTTCC TTCCCGACGC GCTCGCCGTG TGGGACAGCT ACGGGACAA TCTGGAGACC					
GACGACAAGG AAGGGCTGCG CGAGCGGCAC ACCCTGTCGA TGCCGCTGTT AGACCTCTGG					
670	680	690	700	710	720
*	*	*	*	*	*
GGTCTGCGGT ATGGCGGGCA AGGCGCGGTG ATGCTGGAGC CCGGCGTAGT TATCGCCGCG					
CCAGACGCCA TACCGCCCCGT TCCCGGCCAC TACGACCTCG GGCCGCATCA ATAGCGGCAC					
730	740	750	760	770	780
*	*	*	*	*	*
ATGGCCTCGG TGACCGAACAA TCTGGGGCTG GGCGCCACCA TTTCCACCCAC CTACTACCCG					
TACCGGAGCC ACTGGCTTGT AGACCCCCGAC CCGCGGTGGT AAAGGTGGTG GATGATGGGC					
790	800	810	820	830	840
*	*	*	*	*	*
CCCTTACCATG TAGCCCGGGT CGTCGCTTCG CTGGACCAAGC TGTCCTCCGG GCGAGTGTG					
GGGATGGTAC ATCGGGCCCA GCAGCGAACG GACCTGGTCG ACAGGAGGCC CGCTCACAGC					
850	860	870	880	890	900
*	*	*	*	*	*
TGGAACGTGG TCACCTCGCT CAGCAATGCA GAGGCGCGCA ACTTCGGCTT CGATGAACAT					
ACCTTGCACC AGTGGAGCGA GTCGTTACGT CTCCGCGCGT TGAAGCCGAA GCTACTTGTA					
910	920	930	940	950	960
*	*	*	*	*	*
CTCGACCAAGC ATGCCCGCTA CGATCGCGCC GATGAATTCC TCGAGGTCGT GCGCAAGCTC					
GAGCTGGTGC TACGGGCGAT GCTAGCGCGG CTACTTAAGG AGCTCCAGCA CGCGTTCGAG					
970	980	990	1000	1010	1020
*	*	*	*	*	*
TGGAACAGCT GGGATCGCGA TGCGCTGACA CTCGACAAGG CAACCGGCCA GTTCGCCGAT					
ACCTTGTGCA CCCTAGCGCT ACGCGACTGT GAGCTGTTCC GTTGGCCGGT CAAGCGGCTA					
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
CCGGCTAAGG TGCGCTACAT CGACCACCGC GGCAGATGGC TCAACGTACG CGGGCCGCTT					
GGCCGATTCC ACGCGATGTA GCTGGTGGCG CCGCTTACCG AGTTGCATGC GCCCGGGCGAA					
1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
CAGGTGCCGC GCTCCCCCCA GGGCGAGCCT GTCATTCTGC AGGCCGGGCT TTCGGCGCGG					
GTCCACGGCG CGAGGGGGGT CCCGCTCGGA CAGTAAGACG TCCGGCCCGA AAGCCCGCGCC					
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
GGCAAGCGCT TCGCCGGCG CTGGCGGGAC GCGGTGTTCA CGATTCGCC CAATCTGGAC					
CCGTTCGCGA AGCGGCCCGC GACCCGCCTG CGCCACAAAGT GCTAAAGCGG GTTAGACCTG					

FIGURE 6B

*Sphingomonas dsz* sequence (page 3)

1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
ATCATGCAGG CCACGTACCG CGACATAAAG GCGCAGGTCT AGGCCGCCGG ACGCGATCCC					
TAGTACGTCC GGTGCATGGC GCTGTATTC CGCGTCCAGC TCCGGCGGCC TGCGCTAGGG					
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
GAGCAGGTCA AGGTGTTGC CGCGGTGATG CCGATCCTCG GCGAGACCGA GGCGATCGCC					
CTCGTCCAGT TCCACAAACG GCGCCACTAC GGCTAGGAGC CGCTCTGGCT CCGCTAGCGG					
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
AGGCAGCGTC TCGAATACAT AAATTGCGTG GTGCATCCCC AAGTCGGGCT TTCTACGTTG					
TCCGTCGCAG AGCTTATGTA TTTAAGCGAC CACGTAGGGC TTCAGCCCCGA AAGATGCAAC					
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
TCCAGCCATG TCAGGGTCAA CCTTGCCGAC TATTCGCTCG ATACCCCGCT GACCAGGGT					
AGGTCGGTAC AGCCCCAGTT GGAACGGCTG ATAAGCGAGC TATGGGGCGA CTGGCTCCAG					
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
CTGGGGGATC TCGCCCAGCG CAACGTGCC ACCCAAATGG GCATGTTCGC CAGGATGTTG					
GACCCGCTAG AGCGGGTCGC GTTGACAGGG TGGGTTGACC CGTACAAGCG GTCCTACAAC					
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
CAGGCCGAGA CGCTGACCGT GGGAGAAATG GGCCGGCGTT ATGGCGCCAA CGTGGGCTTC					
GTCCGGCTCT GCGACTGGCA CCCTCTTAC CGGGCCGCAA TACCGCGGTT GCACCCGAAG					
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
GTCCCGCAGT GGGCGGGAAC CCGCGAGCAG ATCGCGGACC TGATCGAGAT CCATTCTAACAG					
CAGGGCGTCA CCCGCCCTTG GGCGCTCGTC TAGCGCCTGG ACTAGCTCTA GGTAAAGTTC					
1630	1640	1650	1660	1670	1680
*	*	*	*	*	*
GCCGGCGGCG CCGATGGCTT CATCATCTCG CGGGCGTTCC TGCCCGGATC TTACGAGGAA					
CGGCCGCGCG GGCTACCGAA GTAGTAGAGC GGCGCAAGG ACAGGGCTAG AATGCTCCTT					
1690	1700	1710	1720	1730	1740
*	*	*	*	*	*
TTCGTCGATC AGGTGGTGCC CATCCTGCAG CACCGCGGAC TGTTCCGCAC TGATTACGAA					
AAGCAGCTAG TCCACCACGG GTAGGACGTC GTGGCGCCTG ACAAGGCGTG ACTAATGCTT					
1750	1760	1770	1780	1790	1800
*	*	*	*	*	*
GGCCGCACCC TGCGCAGCCA TCTGGGACTG CGTGAACCG CATACTGGG AGAGTACGCA					
CGGGCGTGGG ACGCGTCGGT AGACCCCTGAC GCACTTGGGC GTATGGACCC TCTCATGCGT					

FIGURE 6C

*Sphingomonas dsz* sequence (page 4)

1810	1820	1830	1840	1850	1860
*	*	*	*	*	*
TGACGACAGA CATCCACCCG GCGAGCGCCG CATCGTCGCC GGCGGCGCGC GCGACGATCA					
ACTGCTGTCT GTAGGTGGGC CGCTCGCGGC GTAGCAGCGG CCGCCGCGCG CGCTGCTAGT					
1870	1880	1890	1900	1910	1920
*	*	*	*	*	*
CCTACAGCAA CTGCCCCGTG CCTAATGCC TGCTCGCCGC GCTCGGCTCA GGTATTCTGG					
GGATGTCGTT GACGGGGCAC GGATTACGGG ACGAGCGCG CGAGCCGAGT CCATAAGACC					
1930	1940	1950	1960	1970	1980
*	*	*	*	*	*
ACAGTGCCGG GATCACACTT GCCCTGCTGA CCGGAAAGCA GGGCGAGGTG CACTTCACCT					
TGTCACTGGCC CTAGTGTGAA CGGGACGACT GGCCTTCGT CCCGCTCCAC GTGAAGTGGA					
1990	2000	2010	2020	2030	2040
*	*	*	*	*	*
ACGACCGAGA TGACTACACC CGCTCGGCCG GCGAGATTCC GCCGCTGGTC AGCGAGGGAC					
TGCTGGCTCT ACTGATGTGG GCGAAGCCGC CGCTCTAAGG CGGCGACCAG TCGCTCCCTG					
2050	2060	2070	2080	2090	2100
*	*	*	*	*	*
TGCCTGCGCC GGGCGGGACC CGCCTGCTGG GACTGACGCC GGTGCTGGGC CGCTGGGGCT					
ACGCACGCGG CCCCGCCTGG CGGGACGACC CTGACTGCCG CCACGACCCCG GCGACCCCGA					
2110	2120	2130	2140	2150	2160
*	*	*	*	*	*
ACTTCGTCCG GGGCGACAGC GCGATCCGCA CCCCAGCCGA TCTTGCCGGC CGCCGCGTCG					
TGAAGCAGGC CCCGCTGTGCG CGCTAGGCGT GGGGCCGGCT AGAACGGCCG GCGCGCAGC					
2170	2180	2190	2200	2210	2220
*	*	*	*	*	*
GAGTATCCGA TTCGGCCAGG AGGATATTGA CCGGAAGGCT GGGGCAACTAC CGCGAACTTG					
CTCATAGGCT AAGCCGGTCC TCCTATAACT GGCCTTCCGA CCCGCTGATG GCGCTTGAAC					
2230	2240	2250	2260	2270	2280
*	*	*	*	*	*
ATCCCCTGGCG CGAGACCCCTG GTCGCGCTGG GGACATGGGA GGGCGGTGCC TTGCTGAGCA					
TAGGGACCGC CGTCTGGGAC CAGCGCGACC CCTGTACCCCT CCGCGCACGG AACGACTCGT					
2290	2300	2310	2320	2330	2340
*	*	*	*	*	*
CGCTCGAGAC GGCAGGGCTT GGCCTCGGCCG ACGTCGAGCT GACGCGCATC GAGAACCCGT					
GCGAGCTCTG CCGCCCCGAA CCGCAGCCGC TGCAGCTCGA CTGCGCGTAG CTCTTGGCA					
2350	2360	2370	2380	2390	2400
*	*	*	*	*	*
TCGTGACGT GCGGACCGAA CGACTGCATG CCGCCGGCTC GCTCAAAGGA ACCGACCTGT					
AGCAGCTGCA CGGCTGGCTT GCTGACGTAC GGCAGCCGAG CGAGTTTCCT TGGCTGGACA					

FIGURE 6D

*Sphingomonas dsz* sequence (page 5)

2410	2420	2430	2440	2450	2460
*	*	*	*	*	*
TCCCCGACGT GACCAGCCAG CAGGCCGCAG TCCTTGAGGA TGAGCGCGCC GACGCCCTGT					
AGGGGCTGCA CTGGTCGGTC GTCCGGCGTC AGGAACTCCT ACTCGCGCGG CTGCGGGACA					
2470	2480	2490	2500	2510	2520
*	*	*	*	*	*
TCGCGTGGCT TCCCCTGGCG GCCGAGCTCG AGACCCGCAT CGGTGCACGG CCGGTCCTAG					
AGCGCACCGA AGGGACCCGC CGGCTCGAGC TCTGGCGTA GCCACGTGCC GGCCAGGATC					
2530	2540	2550	2560	2570	2580
*	*	*	*	*	*
ACCTCAGCGC AGACGACCGC AATGCCTATG CGAGCACCTG GACGGTGAGC GCCGAGCTGG					
TGGAGTCGCG TCTGCTGGCG TTACGGATAAC GCTCGTGGAC CTGCCACTCG CGGCTCGACC					
2590	2600	2610	2620	2630	2640
*	*	*	*	*	*
TGGACCGGGCA GCCCCGAATG GTGCAGCGGC TCGTCGATGC CGTGGTGGAT GCAGGGCGGT					
ACCTGGCCGT CGGGCTTGAC CACGTCGCCG AGCAGCTACG GCACCCACCTA CGTCCCGCCA					
2650	2660	2670	2680	2690	2700
*	*	*	*	*	*
GGGCCGAGGC CAATGGCGAT GTCGTCTCCC GCCTGCACGC CGATAACCTC GGTGTCAGTC					
CCCGGCTCCG GTTACCGCTA CAGCAGAGGG CGGACGTGCG GCTATTGGAG CCACAGTCAG					
2710	2720	2730	2740	2750	2760
*	*	*	*	*	*
CCGAAAGCGT CCGCCAGGGA TTCGGAGCCG ATTTTCACCG CCGCCTGACG CGCGGGCTCG					
GGCTTCGCA GGCGGTCCCT AAGCCTCGGC TAAAAGTGGC GGCGGACTGC GGCGCCGAGC					
2770	2780	2790	2800	2810	2820
*	*	*	*	*	*
ACAGCGATGC TATGCCATC CTGGAGCGTA CTCAGCGGTT CCTGAAGGAT GCGAACCTGA					
TGTGCTACG ATAGCGGTAG GACCTCGCAT GAGTCGCCAA GGACTTCCTA CGCTTGGACT					
2830	2840	2850	2860	2870	2880
*	*	*	*	*	*
TCGATCGGTC GTTGGCGCTC GATCGGTGGG CTGCACCTGA ATTCCCTCGAA CAAAGTCTCT					
AGCTAGCCAG CAACCGCGAG CTAGCCACCC GACGTGGACT TAAGGAGCTT GTTTCAGAGA					
2890	2900	2910	2920	2930	2940
*	*	*	*	*	*
CACGCCAGGT CGAAGGGCAG ATAGCATGAA CGAACCTCGC AAAGATCTCG GCCTCAATCG					
GTGCGGTCCA GCTTCCCGTC TATCGTACTT GCTTGAGCAG TTTCTAGAGC CGGAGTTAGC					
2950	2960	2970	2980	2990	3000
*	*	*	*	*	*
ATCCGATCCG ATCGGCGCTG TCGGGCGACT GGCGCGCGAG TGGGGGGCCA CCCGTGTTGA					
TAGGCTAGGC TAGCCGCGAC ACCCGCGCTGA CGGGCGCGTC ACCCCCCCGGT GGCGACAACT					

FIGURE 6E

*Sphingomonas dsz* sequence (page 6)

3010	3020	3030	3040	3050	3060
*	*	*	*	*	*
TCGGGACCGG GCCGGCGGAT CGGCAACCGC CGAACTCGAT CAACTGCGCG GCAGCGGCCT					
AGCCCTGGCC CGGCCGCCTA GCCGTTGGCG GCTTGAGCTA GTTGACGCCG CGTCGCCGGA					
3070	3080	3090	3100	3110	3120
*	*	*	*	*	*
GCTCTCGCTG TCCATTCCCG CCGCATATGG CGGCTGGGC GCGCACTGGC CAACGACTCT					
CGAGAGCGAC AGGTAAGGGC GGCGTATAACC GCCGACCCCG CGGCTGACCG GTTGCTGAGA					
3130	3140	3150	3160	3170	3180
*	*	*	*	*	*
GGAAGTTATC CGCGAACGTCG CAACGGTGGG CGGATCGCTG GCGCATCTAT TCAGGCTACCA					
CCTTCAATAG GCGCTTCAGC GTTGCCACCT GCCTAGCGAC CGCGTAGATA AGCCGATGGT					
3190	3200	3210	3220	3230	3240
*	*	*	*	*	*
CCTCGGCTGC GTACCGATGTA TCGAGCTGTT CGGCTCGGCG CCACAAAAGG AACGGCTGTA					
GGAGCCGACG CATGGCTACT AGCTCGACAA GCCGAGCCGC GGTGTTTCC TTGCGACAT					
3250	3260	3270	3280	3290	3300
*	*	*	*	*	*
CCGCCAGATC GCAAGCCATG ATTGGCGGGT CGGGAATGCG TCGAGCGAAA ACAACAGCCA					
GGCGGTCTAG CGTTCGGTAC TAACCGCCCCA GCCCTTACGC AGCTCGCTT TGTTGTCGGT					
3310	3320	3330	3340	3350	3360
*	*	*	*	*	*
CGTGCTCGAG TGGAAGCTTG CGGCCACCGC CGTCGATGAT GGCGGGTTCG TCCTCAACGG					
GCACGAGCTC ACCTTCGAAC GGCGGTGGCG CGAGCTACTA CCGCCCAAGC AGGAGTTGCC					
3370	3380	3390	3400	3410	3420
*	*	*	*	*	*
CGCGAACGAC TTCTGCAGCG GCCCCAAAAG CTCCGACCTG CTCATCGTGT TCAGGCGTGT					
GCGCTTCGTG AAGACGTCGC CGCGGTTTTC GAGGCTGGAC GAGTAGCACA AGCCGCACTA					
3430	3440	3450	3460	3470	3480
*	*	*	*	*	*
CCAGGACGAA TCCCCCTGC GCGCGCGAT CATCACCGCG GTCATTCCCA CCGACCGGGC					
GGTCCTGCTT AGGGGGGACG CGCCCGCCTA GTAGTGGCGC CAGTAAGGGT GGCTGGCCCG					
3490	3500	3510	3520	3530	3540
*	*	*	*	*	*
CGGTGTTCAAG ATCAATGACG ACTGGCGCGC AATCGGGATG CGCCAGACCG ACAGCGGCAG					
GCCACAAGTC TAGTTACTGC TGACCGCGCG TTAGCCCTAC GCGGTCTGGC TGTCGCCGTC					
3550	3560	3570	3580	3590	3600
*	*	*	*	*	*
CGCCGAATTG CGCGACGTCC GAGTCTACCC AGACGAGATC TTGGGGGCAC CAAACTCAGT					
GCGGCTTAAA GCGCTGCAGG CTCAGATGGG TCTGCTCTAG AACCCCCGTG GTTTGAGTCA					

FIGURE 6F

*Sphingomonas dsz* sequence (page 7)

3610	3620	3630	3640	3650	3660
*	*	*	*	*	*
CGTTGAGGCG TTCGTGACAA GCAACC CGGG CAGCCT GTGG ACGCCGGCGA TTTCAGTCGAT					
GCAACTCCGC AAGCACTGTT CGTTGGCGCC GTCGGACACC TGCGGCCGCT AAAGTCAGCTA					
3670	3680	3690	3700	3710	3720
*	*	*	*	*	*
CTTCTCGAAC GTTTATCTGG GGCTCGCGCG TGGCGCGCTC GAGGCAGGCGAG CGGATTACAC					
GAAGAGCTTG CAAATAGACC CCGAGCGCGC ACCGCGCGAG CTCCGCGCTC GCCTAATGTG					
3730	3740	3750	3760	3770	3780
*	*	*	*	*	*
CCGGACCCAG AGCCGCCCT GGACACCCCGC CGGCGTGGCG AAGGCGACAG AGGATCCCCA					
GGCCTGGGTC TCGGCGGGGA CCTGTGGCG GCGCACCGC TTCCGCTGTC TCCTAGGGGT					
3790	3800	3810	3820	3830	3840
*	*	*	*	*	*
CATCATCGCC ACCTACGGTG AACTGGCGAT CGCGCTCCAG GGCAGCCGAGG CGGCCGCGCG					
GTAGTAGCGG TGGATGCCAC TTGACCGCTA GCGCGAGGTC CCGCGGGCTCC GCCGGCGCGC					
3850	3860	3870	3880	3890	3900
*	*	*	*	*	*
CGAGGTCGCG GCCCTGTTGC AACAGGCGTG GGACAAGGGC GATGCGGTGA CGCCCGAAGA					
GCTCCAGCGC CGGGACAAACG TTGTCCGCAC CCTGTTCCCG CTACGCCACT GCAGGCTTCT					
3910	3920	3930	3940	3950	3960
*	*	*	*	*	*
GGCGGGCCAG CTGATGGTGA AGGTTTCGGG TGTGAAGGCC CTCTCGACGA AGGCCGCCCT					
CGCGCCGGTC GACTACCACT TCCAAAGCCC ACACCTCCGG GAGAGCTGCT TCCGGCGGGA					
3970	3980	3990	4000	4010	4020
*	*	*	*	*	*
CGACATCACC AGCCGTATTT TCGAGACAAAC GGGCTCGCGA TCGACGCATC CCAGATAACGG					
GCTGTAGTGG TCGGCATAAA AGCTCTGTTG CCCGAGCGCT AGCTGCGTAG GGTCTATGCC					
4030	4040	4050	4060	4070	4080
*	*	*	*	*	*
ATTCGATCGG TTCTGGCGTA ACATCCGGAC TCATACGCTG CACGATCCGG TATCGTATAA					
TAAGCTAGCC AAGACCGCAT TGTAGGCCTG AGTATGCGAC GTGCTAGGCC ATAGCATATT					
4090	4100	4110	4120	4130	4140
*	*	*	*	*	*
AATCGTCGAT GTGGGAACT ACACGCTCAA CGGGACATTC CCGGTTCCCG GATTACGTC					
TTAGCAGCTA CACCCCTTGA TGTGCGAGTT GCCCTGTAAG GGCCAAGGGC CTAAATGCAG					

ATGA  
TACT

FIGURE 6G

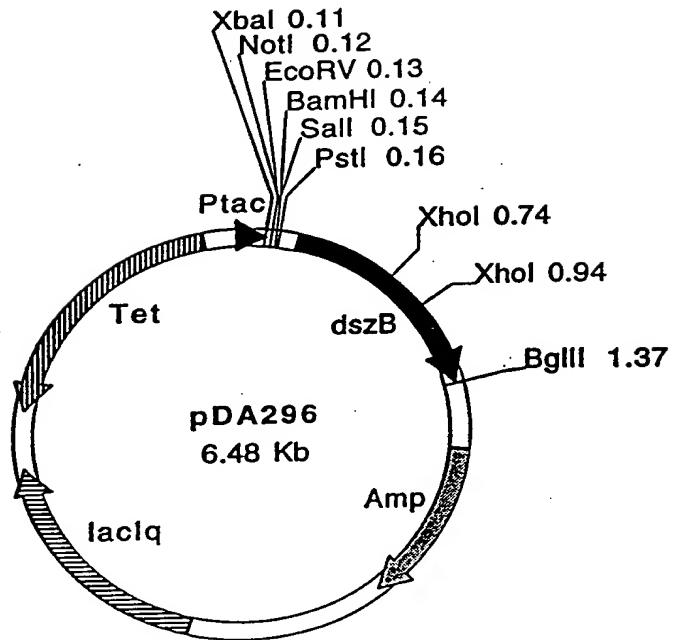


FIGURE 7

DszA (S)	1	MTDPRQLHLAGFFCAGNVTHA GAWR HADDSNGFLTKEYYQQIARTLERG	50
		: .     :     :     :     :     : .     : .     :     :	
DszA (R)	1	MTQQRQMHLAGFFSAGNVTHA GAWR HTDASNDFLSGKYYQHIARTLERG	50
		:     :     :     :     :     : .     : .     :     :	
DszA (S)	51	KFDLLFLPDALAVWDSYGDNLETGLRYGGQAVMLEPGV рIAAMASVTEH	100
		:     :     :     :     : .     : .     : .     : .	
DszA (R)	51	KFDLLFLPDGLAVEDSYGDNLDGVGLGGQAVALEPASVVATMAAVTEH	100
		:     :     :     :     : .     : .     : .     : .	
DszA (S)	101	LGLGATISTTYPPYHVARVVASLDQLSSGRVSWNVVTSLSNAEARNFGF	150
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	101	LGLGATISATYPPYHVARVFATLDQLSGGRVSWNVVTSLNDAEARNFGI	150
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	151	DEHLDHDARYDRADEFLEVVRKLWN SWDRDALTLKD ATGQFADPAKVRYI	200
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	151	NQHLEHDARYDRADEFLEAVKKLWN SWDEDALVLDKAAGVFADPAKVHYV	200
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	201	DHRGEWLNRGPLQVPRSPQGEPVILQAGLSARGKRFAGR WADA VFTISP	250
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	201	DHHGEWLNRGPLQVPRSPQGEPVILQAGLSPRGRRFAGKWA EAVFSLAP	250
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	251	NLDIMQATYRDIIKAQVEAAGRDP EQVKVFAAVMPILGETEAIARORLEYI	300
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	251	NLEVMQATYQGIKAEVDAAGRDPDQT KIFTAVMPVLGESQAVAQERLEYL	300
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	301	NSLVHPEVGLSTLSSHVGVNLAD YSLDTPLTEVLGDLAQRNVPTQLGMFA	350
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	301	NSLVHPEVGLSTLSSHTGINLAAYPLDTPIKDILRDLQDRNVPTQLHMFA	350
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	351	RMLQAETLTVGEMGRRYGANVG FVPQWAGTREQIA D LIEIHFKAGGADGF	400
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	351	AATHSEELTLAEMGRRYGTNVGFVPQWAGTGEQIA DELIRHFEGGAADGF	400
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	401	IISPAFLPGSYEEFVDQVVPILQH RGLFR TDYEGR TLRSHLGLREPAYLG	450
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (R)	401	IISPAFLPGSYDEFVDQVVPVLQDRGYFRTEYQGNTLRDHLGLRV PQLQG	450
		: .     : .     : .     : .     : .     : .     : .     : .	
DszA (S)	451	EYA 453	
		: .	
DszA (R)	451	QPS 453	

FIGURE 8

FIGURE 9

FIGURE 10

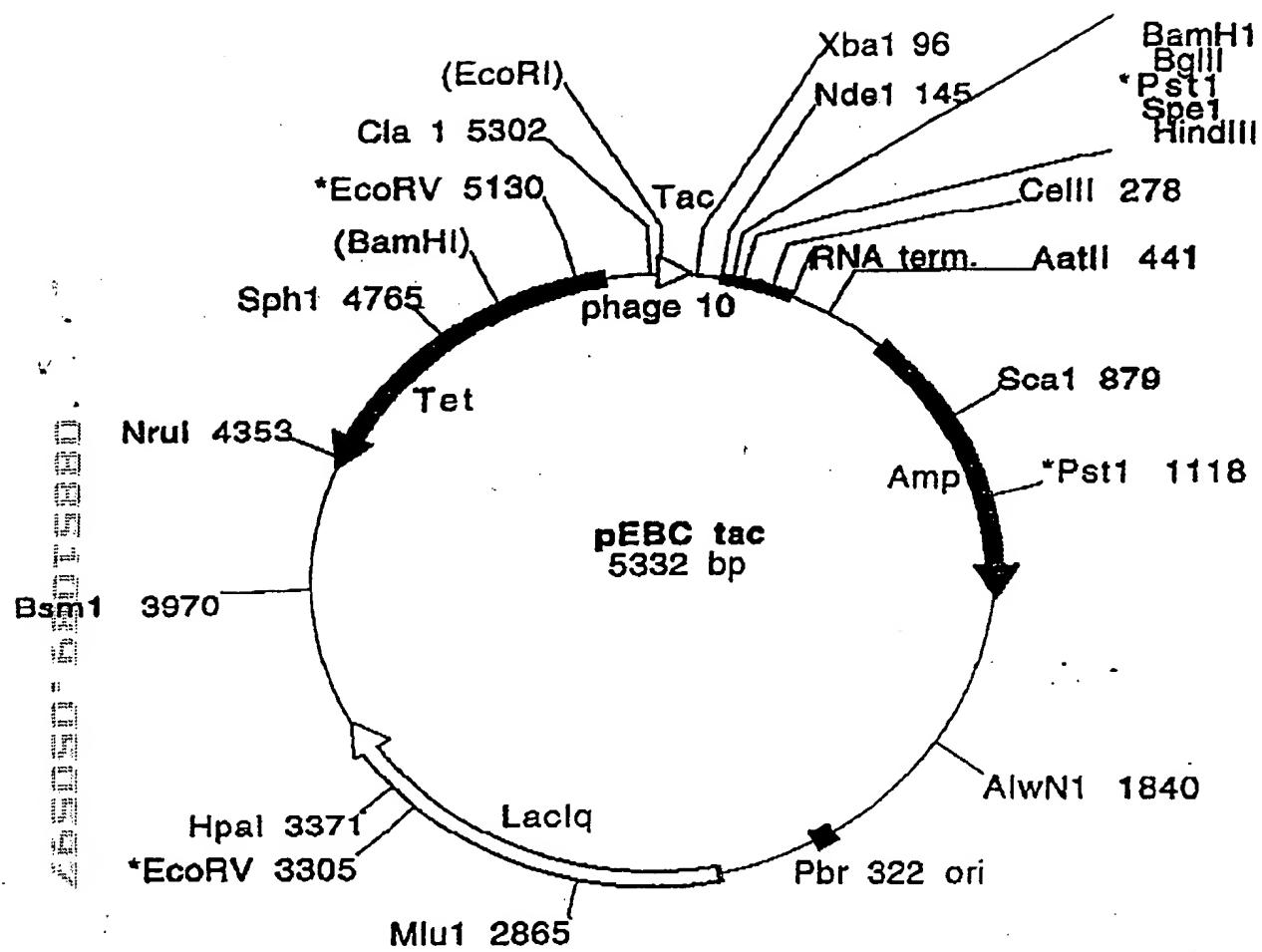


FIGURE 11